Claims

1. Single-stranded oligonucleotide OX, characterized in that it comprises 9 to 42 nucleotides and is capable of hybridizing under mild conditions with an oligonucleotide OY of the sequence Y1-Y2-Y3-Y4-Y5, in which Y1 represents a nucleotide sequence of 1 to 12 nucleotides or Y1 is suppressed, Y2 represents a trinucleotide which codes for Gly, Y3 and Y4 independently represent a trinucleotide which codes for Arg or Lys and Y5 represents a nucleotide sequence of 1 to 21 nucleotides or Y5 is suppressed.

2. Oligonucleotide OX according to claim 1, characterized in that it comprises 9 to 42 nucleotides and is capable of hybridizing under stringent conditions with an oligonucleotide OY of the sequence Y1-Y2-Y3-Y4-Y5, in which Y1 represents a nucleotide sequence of 1 to 12 nucleotides or Y1 is suppressed, Y2 represents a trinucleotide which codes for Gly, Y3 and Y4 independently represent a trinucleotide which codes for Arg or Lys and Y5 represents a nucleotide sequence of 1 to 21 nucleotides or Y5 is suppressed.

3. Oligonucleotide OX according to claim 1 ~~or 2,~~ characterized in that Y1 is suppressed in the oligonucleotide OY.

4. Oligonucleotide OX according to claim 1, ~~2 or 3,~~ characterized in that Y5 is suppressed in the oligonucleotide OY.

5. Oligonucleotide OX according to claim 1, ~~2 or 3,~~ characterized in that, in OY, Y5 represents a nucleotide sequence Y6-Y7-Y8-Y9, in which Y6 represents a trinucleotide which codes for Ser, Thr or Tyr, Y7 represents a trinucleotide which codes for any amino acid, Y8 represents a trinucleotide which codes for Glu or Asp and Y9 represents a nucleotide sequence comprising 1 to 12 nucleotides.

6. Oligonucleotide OX according to claim 5, characterized in that Y1 and Y9 are suppressed in the oligonucleotide OY.

7. Oligonucleotide OX according to claim 6, characterized in that it can hybridize with the said oligonucleotide OY in which Y2 represents a trinucleotide which codes for Gly, Y3 represents a trinucleotide which codes for Lys, Y4 represents a trinucleotide which

codes for Arg and Y5 represents a sequence of 3 trinucleotides which codes for Ser-Ala-Glu.

8. Single-stranded oligonucleotide OY, characterized in that it comprises 9 to 42 nucleotides of the sequence Y1-Y2-Y3-Y4-Y5, in which Y1 represents a nucleotide sequence of 1 to 12 nucleotides or Y1 is suppressed, Y2 represents a trinucleotide which codes for Gly, Y3 and Y4 independently represent a trinucleotide which codes for Arg or Lys and Y5 represents a nucleotide sequence of 1 to 21 nucleotides or Y5 is suppressed.

9. Oligonucleotide OY according to claim 8, characterized in that Y1 is suppressed.

10. Oligonucleotide OY according to claim 8 ~~or 9,~~ characterized in that Y5 is suppressed.

11. Oligonucleotide OY according to claim 8 ~~or 9,~~ characterized in that Y5 represents a nucleotide sequence Y6-Y7-Y8-Y9, in which Y6 represents a trinucleotide which codes for Ser, Thr or Tyr, Y7 represents a trinucleotide which codes for any amino acid, Y8 represents a trinucleotide which codes for Glu or Asp and Y9 represents a nucleotide sequence comprising 1 to 12 nucleotides.

12. Oligonucleotide OY according to claim 11, characterized in that Y1 and Y9 are suppressed.

13. Oligonucleotide OY according to claim 12, characterized in that Y2 represents a trinucleotide which codes for Gly, Y3 represents a trinucleotide which codes for Lys, Y4 represents a trinucleotide which codes for Arg and Y5 represents a sequence of 3 trinucleotides which codes for Ser-Ala-Glu.

14. Single-stranded oligonucleotide OZ, characterized in that it comprises 15 to 39 nucleotides and is capable of hybridizing under mild or stringent conditions with a consensus signal sequence characteristic of amidated polypeptide hormones, the said sequence having as the formula Z1-Z2-Z3-Z4-Z5-Z6-Z7, in which Z1 represents a nucleotide sequence of 1 to 12 nucleotides or Z1 is suppressed, Z2 and Z3 represent two trinucleotides which code for Leu, Z4 and Z5 represent two trinucleotides which code for any two amino acids, Z6 represents a trinucleotide which codes for Leu and Z7 represents a nucleotide sequence of 1 to 12 nucleotides or Z7 is suppressed.

15. Group of oligonucleotides OX according to any one of claims 1 to 7 or of oligonucleotides OZ according to claim 14, characterized in that it constitutes a combinatorial library.

16. Method for identification of the precursor of a peptide having an amidated C-terminal end, characterized by the following successive stages:

- obtaining of a DNA bank;

- hybridization of one or more oligonucleotides according to any one of claims 1 to 7 with the said DNA bank;

- identification of the DNA sequence or sequences of the said bank which hybridizes with an oligonucleotide according to ~~any one of claims 1 to 7~~ claim 1;

- identification in this sequence or sequences of one or more precursors of peptides with a possible amidated C-terminal end.

17. Method according to claim 16, characterized in that the hybridization stage uses a combinatorial library according to claim 15.

18. Method for identification of the precursor of a peptide having an amidated C-terminal end, characterized by the following successive stages:

- obtaining of a DNA bank;

- use of the PCR technique to amplify the fragment of interest with the aid of a group of oligonucleotides according to ~~any one of claims 1 to 7~~ claim 1 and another group of oligonucleotides according to claim 14;

- identification of the DNA sequence or sequences of the said bank which hybridizes with the oligonucleotide according to any one of claims 1 to 7;

- identification in this sequence or sequences of one or more precursors of peptides with a possible amidated C-terminal end.

19. Method according to claim 18, characterized in that the amplification stage uses a combinatorial library according to claim 15.

20. Method for identification of the precursor of a peptide having an amidated C-terminal end, characterized by the following successive stages:

- obtaining of a DNA bank;

- use of the PCR technique to amplify the fragment of interest with the aid of a group of oligonucleotides according to ~~any one of claims 1 to 7~~ claim 1;

- identification of the DNA sequence or sequences of the said bank which hybridizes with the oligonucleotide according to any one of claims 1 to 7;

- identification in this sequence or sequences of one or more precursors of peptides with a possible amidated C-terminal end.

21. Method according to claim 20, characterized in that the amplification stage uses a combinatorial library according to claim 15.

22. Method for identification of the precursor of a polypeptide having an amidated C-terminal end, characterized by the following stages:

- obtaining of a DNA bank;

- use of the PCR technique to amplify the fragment of interest with the aid of an oligonucleotide according to any one of claims 1 to 7 and another single-stranded oligonucleotide capable of hybridizing under mild or stringent conditions with a universal consensus sequence contained in the sequence of the plasmid vector in which the cDNA of the said DNA bank are cloned, such as the primers T3, T7, KS, SK, M13, Reverse;

- identification of the DNA sequence of the said bank which hybridizes with an oligonucleotide according to ~~any one of claims 1 to 7~~ claim 1;

- identification in this sequence of one or more precursors of peptides with a possible amidated C-terminal end.

23. Method according to claim 22, characterized in that the amplification stage uses a combinatorial library according to claim 15.

24. Method according to ~~any one of claims 16 to 23~~ claim 14, characterized in that the DNA bank is cDNA bank.

25. Method according to ~~any one of claims 16 to 24~~ claim 16, characterized in that the single-stranded oligonucleotide can be detected with the aid of a marking agent, such as ^{32}P or digoxigenin.